

SEQUENCE LISTING

<110> Freyssinet, Georges
Rang, Cecile
Frutos, Roger

<120> Pepsin-sensitive modified *Bacillus thuringiensis* insecticidal toxin

<130> A35992-PCT-USA-A (072667.0191)

<140> To Be Assigned

<141> September 19, 2003

<150> PCT/FR02/00772

<151> March 4, 2002

<150> FR 01/03691

<151> March 19, 2001

<160> 160

<170> PatentIn Ver. 2.1

<210> 1

<211> 2019

<212> DNA

<213> *Bacillus thuringiensis*

<220>

<221> CDS

<222> (1)..(2019)

<400> 1

atg aat cga aat aat caa aat gaa tat gaa att att gat gcc ccc cat	48
Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Pro His	
1 5 10 15	
tgt ggg tgt cca tca gat gac gat gtg agg tat cct ttg gca agt gac	96
Cys Gly Cys Pro Ser Asp Asp Asp Val Arg Tyr Pro Leu Ala Ser Asp	
20 25 30	
cca aat gca gcg tta caa aat atg aac tat aaa gat tac tta caa atg	144
Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Gln Met	
35 40 45	
aca gat gag gac tac act gat tct tat ata aat cct agt tta tct att	192
Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu Ser Ile	
50 55 60	
agt ggt aga gat gca gtt cag act gcg ctt act gtt gtt ggg aga ata	240
Ser Gly Arg Asp Ala Val Gln Thr Ala Leu Thr Val Val Gly Arg Ile	
65 70 75 80	
ctc ggg gct tta ggt gtt ccg ttt tct gga caa ata gtg agt ttt tat	288
Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Val Ser Phe Tyr	
85 90 95	

caa ttc ctt tta aat aca ctg tgg cca gtt aat gat aca gct ata tgg	336
Gln Phe Leu Leu Asn Thr Leu Trp Pro Val Asn Asp Thr Ala Ile Trp	
100 105 110	
gaa gct ttc atg cga cag gtg gag gaa ctt gtc aat caa caa ata aca	384
Glu Ala Phe Met Arg Gln Val Glu Glu Leu Val Asn Gln Gln Ile Thr	
115 120 125	
gaa ttt gca aga aat cag gca ctt gca aga ttg caa gga tta gga gac	432
Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Asp	
130 135 140	
tct ttt aat gta tat caa cgt tcc ctt caa aat tgg ttg gct gat cga	480
Ser Phe Asn Val Tyr Gln Arg Ser Leu Gln Asn Trp Leu Ala Asp Arg	
145 150 155 160	
aat gat aca cga aat tta agt gtt gtt cgt gct caa ttt ata gct tta	528
Asn Asp Thr Arg Asn Leu Ser Val Val Arg Ala Gln Phe Ile Ala Leu	
165 170 175	
gac ctt gat ttt gtt aat gct att cca ttg ttt gca gta aat gga cag	576
Asp Leu Asp Phe Val Asn Ala Ile Pro Leu Phe Ala Val Asn Gly Gln	
180 185 190	
cag gtt cca tta ctg tca gta tat gca caa gct gtg aat tta cat ttg	624
Gln Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Val Asn Leu His Leu	
195 200 205	
tta tta tta aaa gat gca tct ctt ttt gga gaa gga tgg gga ttc aca	672
Leu Leu Leu Lys Asp Ala Ser Leu Phe Gly Glu Gly Trp Gly Phe Thr	
210 215 220	
cag ggg gaa att tcc aca tat tat gac cgt caa ttg gaa cta acc gct	720
Gln Gly Glu Ile Ser Thr Tyr Tyr Asp Arg Gln Leu Glu Leu Thr Ala	
225 230 235 240	
aag tac act aat tac tgt gaa act tgg tat aat aca ggt tta gat cgt	768
Lys Tyr Thr Asn Tyr Cys Glu Thr Trp Tyr Asn Thr Gly Leu Asp Arg	
245 250 255	
tta aga gga aca aat act gaa agt tgg tta aga tat cat caa ttc cgt	816
Leu Arg Gly Thr Asn Thr Glu Ser Trp Leu Arg Tyr His Gln Phe Arg	
260 265 270	
aga gaa atg act tta gtg gta tta gat gtt gtg gcg cta ttt cca tat	864
Arg Glu Met Thr Leu Val Val Leu Asp Val Val Ala Leu Phe Pro Tyr	
275 280 285	
tat gat gta cga ctt tat cca acg gga tca aac cca cag ctt aca cgt	912
Tyr Asp Val Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu Thr Arg	
290 295 300	
gag gta tat aca gat ccg att gta ttt aat cca cca gct aat gtt gga	960
Glu Val Tyr Thr Asp Pro Ile Val Phe Asn Pro Pro Ala Asn Val Gly	
305 310 315 320	

ctt tgc cga cgt tgg ggt act aat ccc tat aat act ttt tct gag ctc	1008
Leu Cys Arg Arg Trp Gly Thr Asn Pro Tyr Asn Thr Phe Ser Glu Leu	
325 330 335	
gaa aat gcc ttc att cgc cca cca cat ctt ttt gat agg ctg aat agc	1056
Glu Asn Ala Phe Ile Arg Pro Pro His Leu Phe Asp Arg Leu Asn Ser	
340 345 350	
tta aca atc agc agt aat cga ttt cca gtt tca tct aat ttt atg gat	1104
Leu Thr Ile Ser Ser Asn Arg Phe Pro Val Ser Ser Asn Phe Met Asp	
355 360 365	
tat tgg tca gga cat acg tta cgc cgt agt tat ctg aac gat tca gca	1152
Tyr Trp Ser Gly His Thr Leu Arg Arg Ser Tyr Leu Asn Asp Ser Ala	
370 375 380	
gta caa gaa gat agt tat ggc cta att aca acc aca aga gca aca att	1200
Val Gln Glu Asp Ser Tyr Gly Leu Ile Thr Thr Thr Arg Ala Thr Ile	
385 390 395 400	
aat ccc gga gtt gat gga aca aac cgc ata gag tca acg gca gta gat	1248
Asn Pro Gly Val Asp Gly Thr Asn Arg Ile Glu Ser Thr Ala Val Asp	
405 410 415	
ttt cgt tct gca ttg ata ggt ata tat ggc gtg aat aga gct tct ttt	1296
Phe Arg Ser Ala Leu Ile Gly Ile Tyr Gly Val Asn Arg Ala Ser Phe	
420 425 430	
gtc cca gga ggc ttg ttt aat ggt acg act tct cct gct aat gga gga	1344
Val Pro Gly Gly Leu Phe Asn Gly Thr Thr Ser Pro Ala Asn Gly Gly	
435 440 445	
tgt aga gat ctc tat gat aca aat gat gaa tta cca cca gat gaa agt	1392
Cys Arg Asp Leu Tyr Asp Thr Asn Asp Glu Leu Pro Pro Asp Glu Ser	
450 455 460	
acc gga agt tca acc cat aga cta tct cat gtt acc ttt ttt agc ttt	1440
Thr Gly Ser Ser Thr His Arg Leu Ser His Val Thr Phe Phe Ser Phe	
465 470 475 480	
caa act aat cag gct gga tct ata gct aat gca gga agt gta cct act	1488
Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Val Pro Thr	
485 490 495	
tat gtt tgg acc cgt cgt gat gtg gac ctt aat aat acg att acc cca	1536
Tyr Val Trp Thr Arg Arg Asp Val Asp Leu Asn Asn Thr Ile Thr Pro	
500 505 510	
aat aga att aca caa tta cca ttg gta aag gca tct gca cct gtt tcg	1584
Asn Arg Ile Thr Gln Leu Pro Leu Val Lys Ala Ser Ala Pro Val Ser	
515 520 525	
ggt act acg gtc tta aaa ggt cca gga ttt aca gga ggg ggt ata ctc	1632
Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly Gly Gly Ile Leu	
530 535 540	
cga aga aca act aat ggc aca ttt gga acg tta aga gta acg gtt aat	1680

Arg	Arg	Thr	Thr	Asn	Gly	Thr	Phe	Gly	Thr	Leu	Arg	Val	Thr	Val	Asn	
545					550					555					560	
tca	cca	tta	aca	caa	caa	tat	cgc	cta	aga	gtt	cgt	ttt	gcc	tca	aca	1728
Ser	Pro	Leu	Thr	Gln	Gln	Tyr	Arg	Leu	Arg	Val	Arg	Phe	Ala	Ser	Thr	
				565				570					575			
gga	aat	ttc	agt	ata	agg	gta	ctc	cgt	gga	ggg	gtt	tct	atc	ggg	gat	1776
Gly	Asn	Phe	Ser	Ile	Arg	Val	Leu	Arg	Gly	Gly	Val	Ser	Ile	Gly	Asp	
			580					585					590			
gtt	aga	tta	ggg	agc	aca	atg	aac	aga	ggg	cag	gaa	cta	act	tac	gaa	1824
Val	Arg	Leu	Gly	Ser	Thr	Met	Asn	Arg	Gly	Gln	Glu	Leu	Thr	Tyr	Glu	
		595					600					605				
tcc	ttt	ttc	aca	aga	gag	ttt	act	act	act	ggg	ccg	ttc	aat	ccg	cct	1872
Ser	Phe	Phe	Thr	Arg	Glu	Phe	Thr	Thr	Thr	Gly	Pro	Phe	Asn	Pro	Pro	
	610					615					620					
ttt	aca	ttt	aca	caa	gct	caa	gag	att	cta	aca	gtg	aat	gca	gaa	ggg	1920
Phe	Thr	Phe	Thr	Gln	Ala	Gln	Glu	Ile	Leu	Thr	Val	Asn	Ala	Glu	Gly	
625					630					635				640		
gtt	agc	acc	ggg	ggg	gaa	tat	tat	ata	gat	aga	att	gaa	att	gtc	cct	1968
Val	Ser	Thr	Gly	Gly	Glu	Tyr	Tyr	Ile	Asp	Arg	Ile	Glu	Ile	Val	Pro	
				645					650					655		
gtg	aat	ccg	gca	cga	gaa	gcg	gaa	gag	gat	tta	gaa	gcg	gcg	aag	aaa	2016
Val	Asn	Pro	Ala	Arg	Glu	Ala	Glu	Glu	Asp	Leu	Glu	Ala	Ala	Lys	Lys	
			660					665					670			
gcg																2019
Ala																

<210> 2
 <211> 673
 <212> PRT
 <213> *Bacillus thuringiensis*

<400> 2
 Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Pro His
 1 5 10 15
 Cys Gly Cys Pro Ser Asp Asp Asp Val Arg Tyr Pro Leu Ala Ser Asp
 20 25 30
 Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Gln Met
 35 40 45
 Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu Ser Ile
 50 55 60
 Ser Gly Arg Asp Ala Val Gln Thr Ala Leu Thr Val Val Gly Arg Ile
 65 70 75 80
 Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Val Ser Phe Tyr

85								90				95				
Gln	Phe	Leu	Leu	Asn	Thr	Leu	Trp	Pro	Val	Asn	Asp	Thr	Ala	Ile	Trp	
100								105				110				
Glu	Ala	Phe	Met	Arg	Gln	Val	Glu	Glu	Leu	Val	Asn	Gln	Gln	Ile	Thr	
115								120				125				
Glu	Phe	Ala	Arg	Asn	Gln	Ala	Leu	Ala	Arg	Leu	Gln	Gly	Leu	Gly	Asp	
130								135				140				
Ser	Phe	Asn	Val	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Trp	Leu	Ala	Asp	Arg	
145								150				155				
Asn	Asp	Thr	Arg	Asn	Leu	Ser	Val	Val	Arg	Ala	Gln	Phe	Ile	Ala	Leu	
				165								170				
Asp	Leu	Asp	Phe	Val	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Val	Asn	Gly	Gln	
				180								185				
Gln	Val	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Val	Asn	Leu	His	Leu	
195								200				205				
Leu	Leu	Leu	Lys	Asp	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Trp	Gly	Phe	Thr	
210								215				220				
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Asp	Arg	Gln	Leu	Glu	Leu	Thr	Ala	
225								230				235				
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Trp	Tyr	Asn	Thr	Gly	Leu	Asp	Arg	
				245								250				
Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Trp	Leu	Arg	Tyr	His	Gln	Phe	Arg	
				260								265				
Arg	Glu	Met	Thr	Leu	Val	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Tyr	
275								280				285				
Tyr	Asp	Val	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg	
290								295				300				
Glu	Val	Tyr	Thr	Asp	Pro	Ile	Val	Phe	Asn	Pro	Pro	Ala	Asn	Val	Gly	
305								310				315				
Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu	
				325								330				
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Asp	Arg	Leu	Asn	Ser	
				340								345				
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	Met	Asp	
355								360				365				
Tyr	Trp	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala	
370								375				380				
Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile	

385		390		395		400
Asn Pro Gly Val	Asp Gly Thr	Asn Arg Ile	Glu Ser Thr	Ala Val Asp		
	405		410		415	
Phe Arg Ser Ala	Leu Ile Gly	Ile Tyr Gly	Val Asn Arg	Ala Ser Phe		
	420		425		430	
Val Pro Gly Gly	Leu Phe Asn	Gly Thr Thr	Ser Pro Ala	Asn Gly Gly		
	435		440		445	
Cys Arg Asp Leu	Tyr Asp Thr	Asn Asp Glu	Leu Pro Pro	Asp Glu Ser		
	450		455		460	
Thr Gly Ser Ser	Thr His Arg	Leu Ser His	Val Thr Phe	Phe Ser Phe		
465		470		475		480
Gln Thr Asn Gln	Ala Gly Ser	Ile Ala Asn	Ala Gly Ser	Val Pro Thr		
	485		490		495	
Tyr Val Trp Thr	Arg Arg Asp	Val Asp Leu	Asn Asn Thr	Ile Thr Pro		
	500		505		510	
Asn Arg Ile Thr	Gln Leu Pro	Leu Val Lys	Ala Ser Ala	Pro Val Ser		
	515		520		525	
Gly Thr Thr Val	Leu Lys Gly	Pro Gly Phe	Thr Gly Gly	Gly Ile Leu		
	530		535		540	
Arg Arg Thr Thr	Asn Gly Thr	Phe Gly Thr	Leu Arg Val	Thr Val Asn		
545		550		555		560
Ser Pro Leu Thr	Gln Gln Tyr	Arg Leu Arg	Val Arg Phe	Ala Ser Thr		
	565		570		575	
Gly Asn Phe Ser	Ile Arg Val	Leu Arg Gly	Gly Val Ser	Ile Gly Asp		
	580		585		590	
Val Arg Leu Gly	Ser Thr Met	Asn Arg Gly	Gln Glu Leu	Thr Tyr Glu		
	595		600		605	
Ser Phe Phe Thr	Arg Glu Phe	Thr Thr Thr	Gly Pro Phe	Asn Pro Pro		
	610		615		620	
Phe Thr Phe Thr	Gln Ala Gln	Glu Ile Leu	Thr Val Asn	Ala Glu Gly		
625		630		635		640
Val Ser Thr Gly	Gly Glu Tyr	Tyr Ile Asp	Arg Ile Glu	Ile Val Pro		
	645		650		655	
Val Asn Pro Ala	Arg Glu Ala	Glu Glu Asp	Leu Glu Ala	Ala Lys Lys		
	660		665		670	

Ala

<210> 3
 <211> 2019
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence description: Cry9Ca1 Leu-164

<220>
 <221> CDS
 <222> (1)..(2019)

<400> 3
 atg aat cga aat aat caa aat gaa tat gaa att att gat gcc ccc cat 48
 Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Pro His
 1 5 10 15

tgt ggg tgt cca tca gat gac gat gtg agg tat cct ttg gca agt gac 96
 Cys Gly Cys Pro Ser Asp Asp Asp Val Arg Tyr Pro Leu Ala Ser Asp
 20 25 30

cca aat gca gcg tta caa aat atg aac tat aaa gat tac tta caa atg 144
 Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Gln Met
 35 40 45

aca gat gag gac tac act gat tct tat ata aat cct agt tta tct att 192
 Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu Ser Ile
 50 55 60

agt ggt aga gat gca gtt cag act gcg ctt act gtt gtt ggg aga ata 240
 Ser Gly Arg Asp Ala Val Gln Thr Ala Leu Thr Val Val Gly Arg Ile
 65 70 75 80

ctc ggg gct tta ggt gtt ccg ttt tct gga caa ata gtg agt ttt tat 288
 Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Val Ser Phe Tyr
 85 90 95

caa ttc ctt tta aat aca ctg tgg cca gtt aat gat aca gct ata tgg 336
 Gln Phe Leu Leu Asn Thr Leu Trp Pro Val Asn Asp Thr Ala Ile Trp
 100 105 110

gaa gct ttc atg cga cag gtg gag gaa ctt gtc aat caa caa ata aca 384
 Glu Ala Phe Met Arg Gln Val Glu Glu Leu Val Asn Gln Gln Ile Thr
 115 120 125

gaa ttt gca aga aat cag gca ctt gca aga ttg caa gga tta gga gac 432
 Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Asp
 130 135 140

tct ttt aat gta tat caa cgt tcc ctt caa aat tgg ttg gct gat cga 480
 Ser Phe Asn Val Tyr Gln Arg Ser Leu Gln Asn Trp Leu Ala Asp Arg
 145 150 155 160

aat gat aca tta aat tta agt gtt gtt cgt gct caa ttt ata gct tta 528
 Asn Asp Thr Leu Asn Leu Ser Val Val Arg Ala Gln Phe Ile Ala Leu
 165 170 175

gac ctt gat ttt gtt aat gct att cca ttg ttt gca gta aat gga cag	576
Asp Leu Asp Phe Val Asn Ala Ile Pro Leu Phe Ala Val Asn Gly Gln	
180 185 190	
cag gtt cca tta ctg tca gta tat gca caa gct gtg aat tta cat ttg	624
Gln Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Val Asn Leu His Leu	
195 200 205	
tta tta tta aaa gat gca tct ctt ttt gga gaa gga tgg gga ttc aca	672
Leu Leu Leu Lys Asp Ala Ser Leu Phe Gly Glu Gly Trp Gly Phe Thr	
210 215 220	
cag ggg gaa att tcc aca tat tat gac cgt caa ttg gaa cta acc gct	720
Gln Gly Glu Ile Ser Thr Tyr Tyr Asp Arg Gln Leu Glu Leu Thr Ala	
225 230 235 240	
aag tac act aat tac tgt gaa act tgg tat aat aca ggt tta gat cgt	768
Lys Tyr Thr Asn Tyr Cys Glu Thr Trp Tyr Asn Thr Gly Leu Asp Arg	
245 250 255	
tta aga gga aca aat act gaa agt tgg tta aga tat cat caa ttc cgt	816
Leu Arg Gly Thr Asn Thr Glu Ser Trp Leu Arg Tyr His Gln Phe Arg	
260 265 270	
aga gaa atg act tta gtg gta tta gat gtt gtg gcg cta ttt cca tat	864
Arg Glu Met Thr Leu Val Val Leu Asp Val Val Ala Leu Phe Pro Tyr	
275 280 285	
tat gat gta cga ctt tat cca acg gga tca aac cca cag ctt aca cgt	912
Tyr Asp Val Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu Thr Arg	
290 295 300	
gag gta tat aca gat ccg att gta ttt aat cca cca gct aat gtt gga	960
Glu Val Tyr Thr Asp Pro Ile Val Phe Asn Pro Pro Ala Asn Val Gly	
305 310 315 320	
ctt tgc cga cgt tgg ggt act aat ccc tat aat act ttt tct gag ctc	1008
Leu Cys Arg Arg Trp Gly Thr Asn Pro Tyr Asn Thr Phe Ser Glu Leu	
325 330 335	
gaa aat gcc ttc att cgc cca cca cat ctt ttt gat agg ctg aat agc	1056
Glu Asn Ala Phe Ile Arg Pro Pro His Leu Phe Asp Arg Leu Asn Ser	
340 345 350	
tta aca atc agc agt aat cga ttt cca gtt tca tct aat ttt atg gat	1104
Leu Thr Ile Ser Ser Asn Arg Phe Pro Val Ser Ser Asn Phe Met Asp	
355 360 365	
tat tgg tca gga cat acg tta cgc cgt agt tat ctg aac gat tca gca	1152
Tyr Trp Ser Gly His Thr Leu Arg Arg Ser Tyr Leu Asn Asp Ser Ala	
370 375 380	
gta caa gaa gat agt tat ggc cta att aca acc aca aga gca aca att	1200
Val Gln Glu Asp Ser Tyr Gly Leu Ile Thr Thr Arg Ala Thr Ile	
385 390 395 400	

aat ccc gga gtt gat gga aca aac cgc ata gag tca acg gca gta gat	1248
Asn Pro Gly Val Asp Gly Thr Asn Arg Ile Glu Ser Thr Ala Val Asp	
405 410 415	
ttt cgt tct gca ttg ata ggt ata tat ggc gtg aat aga gct tct ttt	1296
Phe Arg Ser Ala Leu Ile Gly Ile Tyr Gly Val Asn Arg Ala Ser Phe	
420 425 430	
gtc cca gga ggc ttg ttt aat ggt acg act tct cct gct aat gga gga	1344
Val Pro Gly Gly Leu Phe Asn Gly Thr Thr Ser Pro Ala Asn Gly Gly	
435 440 445	
tgt aga gat ctc tat gat aca aat gat gaa tta cca cca gat gaa agt	1392
Cys Arg Asp Leu Tyr Asp Thr Asn Asp Glu Leu Pro Pro Asp Glu Ser	
450 455 460	
acc gga agt tca acc cat aga cta tct cat gtt acc ttt ttt agc ttt	1440
Thr Gly Ser Ser Thr His Arg Leu Ser His Val Thr Phe Phe Ser Phe	
465 470 475 480	
caa act aat cag gct gga tct ata gct aat gca gga agt gta cct act	1488
Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Val Pro Thr	
485 490 495	
tat gtt tgg acc cgt cgt gat gtg gac ctt aat aat acg att acc cca	1536
Tyr Val Trp Thr Arg Arg Asp Val Asp Leu Asn Asn Thr Ile Thr Pro	
500 505 510	
aat aga att aca caa tta cca ttg gta aag gca tct gca cct gtt tcg	1584
Asn Arg Ile Thr Gln Leu Pro Leu Val Lys Ala Ser Ala Pro Val Ser	
515 520 525	
ggg act acg gtc tta aaa ggt cca gga ttt aca gga ggg ggt ata ctc	1632
Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly Gly Gly Ile Leu	
530 535 540	
cga aga aca act aat ggc aca ttt gga acg tta aga gta acg gtt aat	1680
Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Val Thr Val Asn	
545 550 555 560	
tca cca tta aca caa caa tat cgc cta aga gtt cgt ttt gcc tca aca	1728
Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Val Arg Phe Ala Ser Thr	
565 570 575	
gga aat ttc agt ata agg gta ctc cgt gga ggg gtt tct atc ggt gat	1776
Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp	
580 585 590	
gtt aga tta ggg agc aca atg aac aga ggg cag gaa cta act tac gaa	1824
Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu	
595 600 605	
tcc ttt ttc aca aga gag ttt act act act ggt ccg ttc aat ccg cct	1872
Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro	
610 615 620	
ttt aca ttt aca caa gct caa gag att cta aca gtg aat gca gaa ggt	1920

Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly	
625 630 635 640	
gtt agc acc ggt ggt gaa tat tat ata gat aga att gaa att gtc cct	1968
Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro	
645 650 655	
gtg aat ccg gca cga gaa gcg gaa gag gat tta gaa gcg gcg aag aaa	2016
Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Ala Ala Lys Lys	
660 665 670	
gcg	2019
Ala	

<210> 4
 <211> 673
 <212> PRT
 <213> Artificial sequence
 <223> Artificial sequence description: Cry9Ca1 Leu-164

<400> 4	
Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Pro His	
1 5 10 15	
Cys Gly Cys Pro Ser Asp Asp Asp Val Arg Tyr Pro Leu Ala Ser Asp	
20 25 30	
Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Gln Met	
35 40 45	
Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu Ser Ile	
50 55 60	
Ser Gly Arg Asp Ala Val Gln Thr Ala Leu Thr Val Val Gly Arg Ile	
65 70 75 80	
Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Val Ser Phe Tyr	
85 90 95	
Gln Phe Leu Leu Asn Thr Leu Trp Pro Val Asn Asp Thr Ala Ile Trp	
100 105 110	
Glu Ala Phe Met Arg Gln Val Glu Glu Leu Val Asn Gln Gln Ile Thr	
115 120 125	
Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Asp	
130 135 140	
Ser Phe Asn Val Tyr Gln Arg Ser Leu Gln Asn Trp Leu Ala Asp Arg	
145 150 155 160	
Asn Asp Thr Leu Asn Leu Ser Val Val Arg Ala Gln Phe Ile Ala Leu	
165 170 175	
Asp Leu Asp Phe Val Asn Ala Ile Pro Leu Phe Ala Val Asn Gly Gln	
180 185 190	

Gln	Val	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Val	Asn	Leu	His	Leu		
		195					200					205					
Leu	Leu	Leu	Lys	Asp	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Trp	Gly	Phe	Thr		
		210				215					220						
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Asp	Arg	Gln	Leu	Glu	Leu	Thr	Ala		
225					230					235					240		
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Trp	Tyr	Asn	Thr	Gly	Leu	Asp	Arg		
			245						250					255			
Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Trp	Leu	Arg	Tyr	His	Gln	Phe	Arg		
			260					265					270				
Arg	Glu	Met	Thr	Leu	Val	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Tyr		
		275					280					285					
Tyr	Asp	Val	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg		
	290					295					300						
Glu	Val	Tyr	Thr	Asp	Pro	Ile	Val	Phe	Asn	Pro	Pro	Ala	Asn	Val	Gly		
305					310					315					320		
Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu		
				325					330					335			
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Asp	Arg	Leu	Asn	Ser		
			340					345					350				
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	Met	Asp		
		355					360					365					
Tyr	Trp	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala		
	370					375					380						
Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile		
385					390					395					400		
Asn	Pro	Gly	Val	Asp	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Val	Asp		
			405						410					415			
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	Ser	Phe		
			420					425					430				
Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly		
		435					440					445					
Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser		
		450				455					460						
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Val	Thr	Phe	Phe	Ser	Phe		
465					470					475					480		
Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Val	Pro	Thr		
			485					490						495			

Tyr Val Trp Thr Arg Arg Asp Val Asp Leu Asn Asn Thr Ile Thr Pro
 500 505 510
 Asn Arg Ile Thr Gln Leu Pro Leu Val Lys Ala Ser Ala Pro Val Ser
 515 520 525
 Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly Gly Gly Ile Leu
 530 535 540
 Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Val Thr Val Asn
 545 550 555 560
 Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Val Arg Phe Ala Ser Thr
 565 570 575
 Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp
 580 585 590
 Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu
 595 600 605
 Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro
 610 615 620
 Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly
 625 630 635 640
 Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro
 645 650 655
 Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Ala Ala Lys Lys
 660 665 670

Ala

<210> 5
 <211> 2019
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence description: Cry9Ca1 Phe-164

<220>
 <221> CDS
 <222> (1)..(2019)

<400> 5
 atg aat cga aat aat caa aat gaa tat gaa att att gat gcc ccc cat 48
 Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Pro His
 1 5 10 15
 tgt ggg tgt cca tca gat gac gat gtg agg tat cct ttg gca agt gac 96

Cys	Gly	Cys	Pro	Ser	Asp	Asp	Asp	Val	Arg	Tyr	Pro	Leu	Ala	Ser	Asp	
			20					25					30			
cca	aat	gca	gcg	tta	caa	aat	atg	aac	tat	aaa	gat	tac	tta	caa	atg	144
Pro	Asn	Ala	Ala	Leu	Gln	Asn	Met	Asn	Tyr	Lys	Asp	Tyr	Leu	Gln	Met	
		35					40					45				
aca	gat	gag	gac	tac	act	gat	tct	tat	ata	aat	cct	agt	tta	tct	att	192
Thr	Asp	Glu	Asp	Tyr	Thr	Asp	Ser	Tyr	Ile	Asn	Pro	Ser	Leu	Ser	Ile	
	50					55					60					
agt	ggg	aga	gat	gca	gtt	cag	act	gcg	ctt	act	gtt	gtt	ggg	aga	ata	240
Ser	Gly	Arg	Asp	Ala	Val	Gln	Thr	Ala	Leu	Thr	Val	Val	Gly	Arg	Ile	
	65				70				75						80	
ctc	ggg	gct	tta	ggg	gtt	ccg	ttt	tct	gga	caa	ata	gtg	agt	ttt	tat	288
Leu	Gly	Ala	Leu	Gly	Val	Pro	Phe	Ser	Gly	Gln	Ile	Val	Ser	Phe	Tyr	
			85					90						95		
caa	ttc	ctt	tta	aat	aca	ctg	tgg	cca	gtt	aat	gat	aca	gct	ata	tgg	336
Gln	Phe	Leu	Leu	Asn	Thr	Leu	Trp	Pro	Val	Asn	Asp	Thr	Ala	Ile	Trp	
			100					105					110			
gaa	gct	ttc	atg	cga	cag	gtg	gag	gaa	ctt	gtc	aat	caa	caa	ata	aca	384
Glu	Ala	Phe	Met	Arg	Gln	Val	Glu	Glu	Leu	Val	Asn	Gln	Gln	Ile	Thr	
		115					120					125				
gaa	ttt	gca	aga	aat	cag	gca	ctt	gca	aga	ttg	caa	gga	tta	gga	gac	432
Glu	Phe	Ala	Arg	Asn	Gln	Ala	Leu	Ala	Arg	Leu	Gln	Gly	Leu	Gly	Asp	
	130					135					140					
tct	ttt	aat	gta	tat	caa	cgt	tcc	ctt	caa	aat	tgg	ttg	gct	gat	cga	480
Ser	Phe	Asn	Val	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Trp	Leu	Ala	Asp	Arg	
	145				150					155					160	
aat	gat	aca	ttt	aat	tta	agt	gtt	gtt	cgt	gct	caa	ttt	ata	gct	tta	528
Asn	Asp	Thr	Phe	Asn	Leu	Ser	Val	Val	Arg	Ala	Gln	Phe	Ile	Ala	Leu	
				165					170					175		
gac	ctt	gat	ttt	gtt	aat	gct	att	cca	ttg	ttt	gca	gta	aat	gga	cag	576
Asp	Leu	Asp	Phe	Val	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Val	Asn	Gly	Gln	
			180					185					190			
cag	gtt	cca	tta	ctg	tca	gta	tat	gca	caa	gct	gtg	aat	tta	cat	ttg	624
Gln	Val	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Val	Asn	Leu	His	Leu	
		195					200					205				
tta	tta	tta	aaa	gat	gca	tct	ctt	ttt	gga	gaa	gga	tgg	gga	ttc	aca	672
Leu	Leu	Leu	Lys	Asp	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Trp	Gly	Phe	Thr	
	210					215					220					
cag	ggg	gaa	att	tcc	aca	tat	tat	gac	cgt	caa	ttg	gaa	cta	acc	gct	720
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Asp	Arg	Gln	Leu	Glu	Leu	Thr	Ala	
	225				230				235						240	
aag	tac	act	aat	tac	tgt	gaa	act	tgg	tat	aat	aca	ggg	tta	gat	cgt	768
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Trp	Tyr	Asn	Thr	Gly	Leu	Asp	Arg	

245										250					255					
tta	aga	gga	aca	aat	act	gaa	agt	tgg	tta	aga	tat	cat	caa	ttc	cgt	816				
Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Trp	Leu	Arg	Tyr	His	Gln	Phe	Arg					
260					265					270										
aga	gaa	atg	act	tta	gtg	gta	tta	gat	gtt	gtg	gcg	cta	ttt	cca	tat	864				
Arg	Glu	Met	Thr	Leu	Val	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Tyr					
275			280					285												
tat	gat	gta	cga	ctt	tat	cca	acg	gga	tca	aac	cca	cag	ctt	aca	cgt	912				
Tyr	Asp	Val	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg					
290		295					300													
gag	gta	tat	aca	gat	ccg	att	gta	ttt	aat	cca	cca	gct	aat	gtt	gga	960				
Glu	Val	Tyr	Thr	Asp	Pro	Ile	Val	Phe	Asn	Pro	Pro	Ala	Asn	Val	Gly					
305		310					315					320								
ctt	tgc	cga	cgt	tgg	ggg	act	aat	ccc	tat	aat	act	ttt	tct	gag	ctc	1008				
Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu					
325				330					335											
gaa	aat	gcc	ttc	att	cgc	cca	cca	cat	ctt	ttt	gat	agg	ctg	aat	agc	1056				
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Asp	Arg	Leu	Asn	Ser					
340				345					350											
tta	aca	atc	agc	agt	aat	cga	ttt	cca	gtt	tca	tct	aat	ttt	atg	gat	1104				
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	Met	Asp					
355			360					365												
tat	tgg	tca	gga	cat	acg	tta	cgc	cgt	agt	tat	ctg	aac	gat	tca	gca	1152				
Tyr	Trp	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala					
370		375					380													
gta	caa	gaa	gat	agt	tat	ggc	cta	att	aca	acc	aca	aga	gca	aca	att	1200				
Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile					
385		390					395					400								
aat	ccc	gga	gtt	gat	gga	aca	aac	cgc	ata	gag	tca	acg	gca	gta	gat	1248				
Asn	Pro	Gly	Val	Asp	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Val	Asp					
405				410					415											
ttt	cgt	tct	gca	ttg	ata	ggg	ata	tat	ggc	gtg	aat	aga	gct	tct	ttt	1296				
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	Ser	Phe					
420			425					430												
gtc	cca	gga	ggc	ttg	ttt	aat	ggg	acg	act	tct	cct	gct	aat	gga	gga	1344				
Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly					
435			440					445												
tgt	aga	gat	ctc	tat	gat	aca	aat	gat	gaa	tta	cca	cca	gat	gaa	agt	1392				
Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser					
450		455					460													
acc	gga	agt	tca	acc	cat	aga	cta	tct	cat	gtt	acc	ttt	ttt	agc	ttt	1440				
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Val	Thr	Phe	Phe	Ser	Phe					
465		470					475					480								

caa act aat cag gct gga tct ata gct aat gca gga agt gta cct act	1488
Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Val Pro Thr	
485 490 495	
tat gtt tgg acc cgt cgt gat gtg gac ctt aat aat acg att acc cca	1536
Tyr Val Trp Thr Arg Arg Asp Val Asp Leu Asn Asn Thr Ile Thr Pro	
500 505 510	
aat aga att aca caa tta cca ttg gta aag gca tct gca cct gtt tcg	1584
Asn Arg Ile Thr Gln Leu Pro Leu Val Lys Ala Ser Ala Pro Val Ser	
515 520 525	
ggg act acg gtc tta aaa ggt cca gga ttt aca gga ggg ggt ata ctc	1632
Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly Gly Gly Ile Leu	
530 535 540	
cga aga aca act aat ggc aca ttt gga acg tta aga gta acg gtt aat	1680
Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Val Thr Val Asn	
545 550 555 560	
tca cca tta aca caa caa tat cgc cta aga gtt cgt ttt gcc tca aca	1728
Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Val Arg Phe Ala Ser Thr	
565 570 575	
gga aat ttc agt ata agg gta ctc cgt gga ggg gtt tct atc ggt gat	1776
Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp	
580 585 590	
gtt aga tta ggg agc aca atg aac aga ggg cag gaa cta act tac gaa	1824
Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu	
595 600 605	
tcc ttt ttc aca aga gag ttt act act act ggt ccg ttc aat ccg cct	1872
Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro	
610 615 620	
ttt aca ttt aca caa gct caa gag att cta aca gtg aat gca gaa ggt	1920
Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly	
625 630 635 640	
gtt agc acc ggt ggt gaa tat tat ata gat aga att gaa att gtc cct	1968
Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro	
645 650 655	
gtg aat ccg gca cga gaa gcg gaa gag gat tta gaa gcg gcg aag aaa	2016
Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Ala Ala Lys Lys	
660 665 670	
gcg	2019
Ala	

<210> 6

<211> 673

<212> PRT

<213> Artificial sequence

<223> Artificial sequence description: Cry9Ca1 Phe-164

<400> 6

Met	Asn	Arg	Asn	Asn	Gln	Asn	Glu	Tyr	Glu	Ile	Ile	Asp	Ala	Pro	His	
1				5					10					15		
Cys	Gly	Cys	Pro	Ser	Asp	Asp	Asp	Val	Arg	Tyr	Pro	Leu	Ala	Ser	Asp	
			20					25					30			
Pro	Asn	Ala	Ala	Leu	Gln	Asn	Met	Asn	Tyr	Lys	Asp	Tyr	Leu	Gln	Met	
		35					40					45				
Thr	Asp	Glu	Asp	Tyr	Thr	Asp	Ser	Tyr	Ile	Asn	Pro	Ser	Leu	Ser	Ile	
	50					55					60					
Ser	Gly	Arg	Asp	Ala	Val	Gln	Thr	Ala	Leu	Thr	Val	Val	Gly	Arg	Ile	
65					70					75					80	
Leu	Gly	Ala	Leu	Gly	Val	Pro	Phe	Ser	Gly	Gln	Ile	Val	Ser	Phe	Tyr	
				85					90					95		
Gln	Phe	Leu	Leu	Asn	Thr	Leu	Trp	Pro	Val	Asn	Asp	Thr	Ala	Ile	Trp	
		100						105					110			
Glu	Ala	Phe	Met	Arg	Gln	Val	Glu	Glu	Leu	Val	Asn	Gln	Gln	Ile	Thr	
	115						120					125				
Glu	Phe	Ala	Arg	Asn	Gln	Ala	Leu	Ala	Arg	Leu	Gln	Gly	Leu	Gly	Asp	
	130					135					140					
Ser	Phe	Asn	Val	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Trp	Leu	Ala	Asp	Arg	
145					150					155					160	
Asn	Asp	Thr	Phe	Asn	Leu	Ser	Val	Val	Arg	Ala	Gln	Phe	Ile	Ala	Leu	
				165					170					175		
Asp	Leu	Asp	Phe	Val	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Val	Asn	Gly	Gln	
		180						185					190			
Gln	Val	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Val	Asn	Leu	His	Leu	
	195						200					205				
Leu	Leu	Leu	Lys	Asp	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Trp	Gly	Phe	Thr	
	210					215						220				
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Asp	Arg	Gln	Leu	Glu	Leu	Thr	Ala	
225					230					235					240	
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Trp	Tyr	Asn	Thr	Gly	Leu	Asp	Arg	
			245						250					255		
Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Trp	Leu	Arg	Tyr	His	Gln	Phe	Arg	
		260						265					270			
Arg	Glu	Met	Thr	Leu	Val	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Tyr	
	275						280					285				

Tyr	Asp	Val	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg
290						295					300				
Glu	Val	Tyr	Thr	Asp	Pro	Ile	Val	Phe	Asn	Pro	Pro	Ala	Asn	Val	Gly
305					310				315						320
Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu
				325					330					335	
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Asp	Arg	Leu	Asn	Ser
			340					345					350		
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	Met	Asp
		355					360					365			
Tyr	Trp	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala
	370					375					380				
Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile
385					390					395					400
Asn	Pro	Gly	Val	Asp	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Val	Asp
				405					410					415	
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	Ser	Phe
			420					425					430		
Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly
		435					440					445			
Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser
	450					455					460				
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Val	Thr	Phe	Phe	Ser	Phe
465					470					475					480
Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Val	Pro	Thr
				485					490					495	
Tyr	Val	Trp	Thr	Arg	Arg	Asp	Val	Asp	Leu	Asn	Asn	Thr	Ile	Thr	Pro
			500					505					510		
Asn	Arg	Ile	Thr	Gln	Leu	Pro	Leu	Val	Lys	Ala	Ser	Ala	Pro	Val	Ser
		515					520					525			
Gly	Thr	Thr	Val	Leu	Lys	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Gly	Ile	Leu
		530				535					540				
Arg	Arg	Thr	Thr	Asn	Gly	Thr	Phe	Gly	Thr	Leu	Arg	Val	Thr	Val	Asn
545					550					555					560
Ser	Pro	Leu	Thr	Gln	Gln	Tyr	Arg	Leu	Arg	Val	Arg	Phe	Ala	Ser	Thr
				565					570					575	
Gly	Asn	Phe	Ser	Ile	Arg	Val	Leu	Arg	Gly	Gly	Val	Ser	Ile	Gly	Asp
			580					585					590		

Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu
595 600 605

Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro
610 615 620

Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly
625 630 635 640

Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro
645 650 655

Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Ala Ala Lys Lys
660 665 670

Ala

<210> 7

<211> 2019

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: Cry9Ca1 Glu-164

<220>

<221> CDS

<222> (1)..(2019)

<400> 7

atg aat cga aat aat caa aat gaa tat gaa att att gat gcc ccc cat	48
Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Pro His	
1 5 10 15	

tgt ggg tgt cca tca gat gac gat gtg agg tat cct ttg gca agt gac	96
Cys Gly Cys Pro Ser Asp Asp Asp Val Arg Tyr Pro Leu Ala Ser Asp	
20 25 30	

cca aat gca gcg tta caa aat atg aac tat aaa gat tac tta caa atg	144
Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Gln Met	
35 40 45	

aca gat gag gac tac act gat tct tat ata aat cct agt tta tct att	192
Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu Ser Ile	
50 55 60	

agt ggt aga gat gca gtt cag act gcg ctt act gtt gtt ggg aga ata	240
Ser Gly Arg Asp Ala Val Gln Thr Ala Leu Thr Val Val Gly Arg Ile	
65 70 75 80	

ctc ggg gct tta ggt gtt ccg ttt tct gga caa ata gtg agt ttt tat	288
Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Val Ser Phe Tyr	
85 90 95	

caa ttc ctt tta aat aca ctg tgg cca gtt aat gat aca gct ata tgg	336
Gln Phe Leu Leu Asn Thr Leu Trp Pro Val Asn Asp Thr Ala Ile Trp	
100 105 110	
gaa gct ttc atg cga cag gtg gag gaa ctt gtc aat caa caa ata aca	384
Glu Ala Phe Met Arg Gln Val Glu Glu Leu Val Asn Gln Gln Ile Thr	
115 120 125	
gaa ttt gca aga aat cag gca ctt gca aga ttg caa gga tta gga gac	432
Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Asp	
130 135 140	
tct ttt aat gta tat caa cgt tcc ctt caa aat tgg ttg gct gat cga	480
Ser Phe Asn Val Tyr Gln Arg Ser Leu Gln Asn Trp Leu Ala Asp Arg	
145 150 155 160	
aat gat aca gaa aat tta agt gtt gtt cgt gct caa ttt ata gct tta	528
Asn Asp Thr Glu Asn Leu Ser Val Val Arg Ala Gln Phe Ile Ala Leu	
165 170 175	
gac ctt gat ttt gtt aat gct att cca ttg ttt gca gta aat gga cag	576
Asp Leu Asp Phe Val Asn Ala Ile Pro Leu Phe Ala Val Asn Gly Gln	
180 185 190	
cag gtt cca tta ctg tca gta tat gca caa gct gtg aat tta cat ttg	624
Gln Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Val Asn Leu His Leu	
195 200 205	
tta tta tta aaa gat gca tct ctt ttt gga gaa gga tgg gga ttc aca	672
Leu Leu Leu Lys Asp Ala Ser Leu Phe Gly Glu Gly Trp Gly Phe Thr	
210 215 220	
cag ggg gaa att tcc aca tat tat gac cgt caa ttg gaa cta acc gct	720
Gln Gly Glu Ile Ser Thr Tyr Tyr Asp Arg Gln Leu Glu Leu Thr Ala	
225 230 235 240	
aag tac act aat tac tgt gaa act tgg tat aat aca ggt tta gat cgt	768
Lys Tyr Thr Asn Tyr Cys Glu Thr Trp Tyr Asn Thr Gly Leu Asp Arg	
245 250 255	
tta aga gga aca aat act gaa agt tgg tta aga tat cat caa ttc cgt	816
Leu Arg Gly Thr Asn Thr Glu Ser Trp Leu Arg Tyr His Gln Phe Arg	
260 265 270	
aga gaa atg act tta gtg gta tta gat gtt gtg gcg cta ttt cca tat	864
Arg Glu Met Thr Leu Val Val Leu Asp Val Val Ala Leu Phe Pro Tyr	
275 280 285	
tat gat gta cga ctt tat cca acg gga tca aac cca cag ctt aca cgt	912
Tyr Asp Val Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu Thr Arg	
290 295 300	
gag gta tat aca gat ccg att gta ttt aat cca cca gct aat gtt gga	960
Glu Val Tyr Thr Asp Pro Ile Val Phe Asn Pro Pro Ala Asn Val Gly	
305 310 315 320	
ctt tgc cga cgt tgg ggt act aat ccc tat aat act ttt tct gag ctc	1008

Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu	
				325					330					335		
gaa	aat	gcc	ttc	att	cgc	cca	cca	cat	ctt	ttt	gat	agg	ctg	aat	agc	1056
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Asp	Arg	Leu	Asn	Ser	
			340					345					350			
tta	aca	atc	agc	agt	aat	cga	ttt	cca	gtt	tca	tct	aat	ttt	atg	gat	1104
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	Met	Asp	
			355				360						365			
tat	tgg	tca	gga	cat	acg	tta	cgc	cgt	agt	tat	ctg	aac	gat	tca	gca	1152
Tyr	Trp	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala	
	370					375					380					
gta	caa	gaa	gat	agt	tat	ggc	cta	att	aca	acc	aca	aga	gca	aca	att	1200
Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile	
	385				390					395					400	
aat	ccc	gga	gtt	gat	gga	aca	aac	cgc	ata	gag	tca	acg	gca	gta	gat	1248
Asn	Pro	Gly	Val	Asp	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Val	Asp	
				405					410					415		
ttt	cgt	tct	gca	ttg	ata	ggg	ata	tat	ggc	gtg	aat	aga	gct	tct	ttt	1296
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	Ser	Phe	
			420					425					430			
gtc	cca	gga	ggc	ttg	ttt	aat	ggg	acg	act	tct	cct	gct	aat	gga	gga	1344
Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly	
		435					440					445				
tgt	aga	gat	ctc	tat	gat	aca	aat	gat	gaa	tta	cca	cca	gat	gaa	agt	1392
Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser	
	450					455					460					
acc	gga	agt	tca	acc	cat	aga	cta	tct	cat	gtt	acc	ttt	ttt	agc	ttt	1440
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Val	Thr	Phe	Phe	Ser	Phe	
	465				470					475					480	
caa	act	aat	cag	gct	gga	tct	ata	gct	aat	gca	gga	agt	gta	cct	act	1488
Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Val	Pro	Thr	
			485					490					495			
tat	gtt	tgg	acc	cgt	cgt	gat	gtg	gac	ctt	aat	aat	acg	att	acc	cca	1536
Tyr	Val	Trp	Thr	Arg	Arg	Asp	Val	Asp	Leu	Asn	Asn	Thr	Ile	Thr	Pro	
			500					505					510			
aat	aga	att	aca	caa	tta	cca	ttg	gta	aag	gca	tct	gca	cct	gtt	tcg	1584
Asn	Arg	Ile	Thr	Gln	Leu	Pro	Leu	Val	Lys	Ala	Ser	Ala	Pro	Val	Ser	
		515					520					525				
ggg	act	acg	gtc	tta	aaa	ggg	cca	gga	ttt	aca	gga	ggg	ggg	ata	ctc	1632
Gly	Thr	Thr	Val	Leu	Lys	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Gly	Ile	Leu	
	530					535					540					
cga	aga	aca	act	aat	ggc	aca	ttt	gga	acg	tta	aga	gta	acg	gtt	aat	1680
Arg	Arg	Thr	Thr	Asn	Gly	Thr	Phe	Gly	Thr	Leu	Arg	Val	Thr	Val	Asn	

545	550	555	560	
tca cca tta aca caa caa tat cgc cta aga gtt cgt ttt gcc tca aca				1728
Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Val Arg Phe Ala Ser Thr	565	570	575	
gga aat ttc agt ata agg gta ctc cgt gga ggg gtt tct atc ggt gat				1776
Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp	580	585	590	
gtt aga tta ggg agc aca atg aac aga ggg cag gaa cta act tac gaa				1824
Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu	595	600	605	
tcc ttt ttc aca aga gag ttt act act act ggt ccg ttc aat ccg cct				1872
Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro	610	615	620	
ttt aca ttt aca caa gct caa gag att cta aca gtg aat gca gaa ggt				1920
Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly	625	630	640	
gtt agc acc ggt ggt gaa tat tat ata gat aga att gaa att gtc cct				1968
Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro	645	650	655	
gtg aat ccg gca cga gaa gcg gaa gag gat tta gaa gcg gcg aag aaa				2016
Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Ala Ala Lys Lys	660	665	670	
gcg				2019
Ala				

<210> 8
 <211> 673
 <212> PRT
 <213> Artificial sequence
 <223> Artificial sequence description: Cry9Ca1 Glu-164

<400> 8	
Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Pro His	
1 5 10 15	
Cys Gly Cys Pro Ser Asp Asp Asp Val Arg Tyr Pro Leu Ala Ser Asp	
20 25 30	
Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Gln Met	
35 40 45	
Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu Ser Ile	
50 55 60	
Ser Gly Arg Asp Ala Val Gln Thr Ala Leu Thr Val Val Gly Arg Ile	
65 70 75 80	
Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Val Ser Phe Tyr	

85					90					95					
Gln	Phe	Leu	Leu	Asn	Thr	Leu	Trp	Pro	Val	Asn	Asp	Thr	Ala	Ile	Trp
		100						105					110		
Glu	Ala	Phe	Met	Arg	Gln	Val	Glu	Glu	Leu	Val	Asn	Gln	Gln	Ile	Thr
		115					120					125			
Glu	Phe	Ala	Arg	Asn	Gln	Ala	Leu	Ala	Arg	Leu	Gln	Gly	Leu	Gly	Asp
		130				135					140				
Ser	Phe	Asn	Val	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Trp	Leu	Ala	Asp	Arg
145					150					155					160
Asn	Asp	Thr	Glu	Asn	Leu	Ser	Val	Val	Arg	Ala	Gln	Phe	Ile	Ala	Leu
				165					170					175	
Asp	Leu	Asp	Phe	Val	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Val	Asn	Gly	Gln
			180					185						190	
Gln	Val	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Val	Asn	Leu	His	Leu
		195					200					205			
Leu	Leu	Leu	Lys	Asp	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Trp	Gly	Phe	Thr
	210					215					220				
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Asp	Arg	Gln	Leu	Glu	Leu	Thr	Ala
225					230					235					240
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Trp	Tyr	Asn	Thr	Gly	Leu	Asp	Arg
			245						250					255	
Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Trp	Leu	Arg	Tyr	His	Gln	Phe	Arg
			260					265					270		
Arg	Glu	Met	Thr	Leu	Val	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Tyr
		275					280					285			
Tyr	Asp	Val	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg
	290					295					300				
Glu	Val	Tyr	Thr	Asp	Pro	Ile	Val	Phe	Asn	Pro	Pro	Ala	Asn	Val	Gly
305					310					315					320
Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu
				325					330					335	
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Asp	Arg	Leu	Asn	Ser
			340					345					350		
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	Met	Asp
		355					360					365			
Tyr	Trp	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala
	370					375					380				
Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile

385		390		395		400
Asn Pro Gly Val	Asp Gly Thr	Asn Arg Ile	Glu Ser Thr	Ala Val Asp		
	405		410		415	
Phe Arg Ser Ala	Leu Ile Gly	Ile Tyr Gly	Val Asn Arg	Ala Ser Phe		
	420		425		430	
Val Pro Gly Gly	Leu Phe Asn	Gly Thr Thr	Ser Pro Ala	Asn Gly Gly		
	435		440		445	
Cys Arg Asp Leu	Tyr Asp Thr	Asn Asp Glu	Leu Pro Pro	Asp Glu Ser		
	450		455		460	
Thr Gly Ser Ser	Thr His Arg	Leu Ser His	Val Thr Phe	Phe Ser Phe		
465		470		475		480
Gln Thr Asn Gln	Ala Gly Ser	Ile Ala Asn	Ala Gly Ser	Val Pro Thr		
	485		490		495	
Tyr Val Trp Thr	Arg Arg Asp	Val Asp Leu	Asn Asn Thr	Ile Thr Pro		
	500		505		510	
Asn Arg Ile Thr	Gln Leu Pro	Leu Val Lys	Ala Ser Ala	Pro Val Ser		
	515		520		525	
Gly Thr Thr Val	Leu Lys Gly	Pro Gly Phe	Thr Gly Gly	Gly Ile Leu		
	530		535		540	
Arg Arg Thr Thr	Asn Gly Thr	Phe Gly Thr	Leu Arg Val	Thr Val Asn		
545		550		555		560
Ser Pro Leu Thr	Gln Gln Tyr	Arg Leu Arg	Val Arg Phe	Ala Ser Thr		
	565		570		575	
Gly Asn Phe Ser	Ile Arg Val	Leu Arg Gly	Gly Val Ser	Ile Gly Asp		
	580		585		590	
Val Arg Leu Gly	Ser Thr Met	Asn Arg Gly	Gln Glu Leu	Thr Tyr Glu		
	595		600		605	
Ser Phe Phe Thr	Arg Glu Phe	Thr Thr Thr	Gly Pro Phe	Asn Pro Pro		
	610		615		620	
Phe Thr Phe Thr	Gln Ala Gln	Glu Ile Leu	Thr Val Asn	Ala Glu Gly		
625		630		635		640
Val Ser Thr Gly	Gly Glu Tyr	Tyr Ile Asp	Arg Ile Glu	Ile Val Pro		
	645		650		655	
Val Asn Pro Ala	Arg Glu Ala	Glu Glu Asp	Leu Glu Ala	Ala Lys Lys		
	660		665		670	

Ala

<210> 9
 <211> 2019
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence description: Cry9Ca1-100%

<220>
 <221> CDS
 <222> (1)..(2019)

<400> 9
 atg aat cga aat aat caa aat gaa tat gaa att att gaa gcc ccc cat 48
 Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Glu Ala Pro His
 1 5 10 15

tgt ggg tgt cca tca gaa gaa gaa tta agg tat cct ttg gca agt gaa 96
 Cys Gly Cys Pro Ser Glu Glu Glu Leu Arg Tyr Pro Leu Ala Ser Glu
 20 25 30

cca aat gca gcg tta caa aat atg aac tat aaa gaa tac tta caa atg 144
 Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Glu Tyr Leu Gln Met
 35 40 45

aca gaa gag gaa tac act gaa tct tat ata aat cct agt tta tct att 192
 Thr Glu Glu Glu Tyr Thr Glu Ser Tyr Ile Asn Pro Ser Leu Ser Ile
 50 55 60

agt ggt aga gaa gca tta cag act gcg ctt act gtt att agg aga ata 240
 Ser Gly Arg Glu Ala Leu Gln Thr Ala Leu Thr Val Ile Arg Arg Ile
 65 70 75 80

ctc ggg gct tta ggt tta ccg ttt tct gga caa ata tta agt ttt tat 288
 Leu Gly Ala Leu Gly Leu Pro Phe Ser Gly Gln Ile Leu Ser Phe Tyr
 85 90 95

caa ttc ctt tta aat aca ctg ttt cca tta aat gaa aca gct ata ttt 336
 Gln Phe Leu Leu Asn Thr Leu Phe Pro Leu Asn Glu Thr Ala Ile Phe
 100 105 110

gaa gct ttc atg cga cag tta gag gaa ctt tta aat caa caa ata aca 384
 Glu Ala Phe Met Arg Gln Leu Glu Glu Leu Leu Asn Gln Gln Ile Thr
 115 120 125

gaa ttt gca aga aat cag gca ctt gca aga ttg caa gga tta gga gaa 432
 Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Glu
 130 135 140

tct ttt aat tta tat caa cgt tcc ctt caa aat ttt ttg gct gaa cga 480
 Ser Phe Asn Leu Tyr Gln Arg Ser Leu Gln Asn Phe Leu Ala Glu Arg
 145 150 155 160

aat gaa aca cga aat tta agt tta tta cgt gct caa ttt ata gct tta 528
 Asn Glu Thr Arg Asn Leu Ser Leu Leu Arg Ala Gln Phe Ile Ala Leu
 165 170 175

gaa ctt gaa ttt tta aat gct att cca ttg ttt gca tta aat gga cag	576
Glu Leu Glu Phe Leu Asn Ala Ile Pro Leu Phe Ala Leu Asn Gly Gln	
180 185 190	
cag tta cca tta ctg tca tta tat gca caa gct tta aat tta cat ttg	624
Gln Leu Pro Leu Leu Ser Leu Tyr Ala Gln Ala Leu Asn Leu His Leu	
195 200 205	
tta tta tta aaa gaa gca tct ctt ttt gga gaa gga ttt gga ttc aca	672
Leu Leu Leu Lys Glu Ala Ser Leu Phe Gly Glu Gly Phe Gly Phe Thr	
210 215 220	
cag ggg gaa att tcc aca tat tat gaa cgt caa ttg gaa cta acc gct	720
Gln Gly Glu Ile Ser Thr Tyr Tyr Glu Arg Gln Leu Glu Leu Thr Ala	
225 230 235 240	
aag tac act aat tac tgt gaa act ttt tat aat aca ggt tta gaa cgt	768
Lys Tyr Thr Asn Tyr Cys Glu Thr Phe Tyr Asn Thr Gly Leu Glu Arg	
245 250 255	
tta aga gga aca aat act gaa agt ttt tta aga tat cat caa ttc cgt	816
Leu Arg Gly Thr Asn Thr Glu Ser Phe Leu Arg Tyr His Gln Phe Arg	
260 265 270	
aga gaa atg act tta tta tta tta gaa tta tta gcg cta ttt cca tat	864
Arg Glu Met Thr Leu Leu Leu Leu Glu Leu Leu Ala Leu Phe Pro Tyr	
275 280 285	
tat gaa tta cga ctt tat cca acg gga tca aac cca cag ctt aca cgt	912
Tyr Glu Leu Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu Thr Arg	
290 295 300	
gag tta tat aca gaa ccg att tta ttt aat cca cca gct aat tta gga	960
Glu Leu Tyr Thr Glu Pro Ile Leu Phe Asn Pro Pro Ala Asn Leu Gly	
305 310 315 320	
ctt tgc cga cgt ttt ggt act aat ccc tat aat act ttt tct gag ctc	1008
Leu Cys Arg Arg Phe Gly Thr Asn Pro Tyr Asn Thr Phe Ser Glu Leu	
325 330 335	
gaa aat gcc ttc att cgc cca cca cat ctt ttt gaa agg ctg aat agc	1056
Glu Asn Ala Phe Ile Arg Pro Pro His Leu Phe Glu Arg Leu Asn Ser	
340 345 350	
tta aca atc agc agt aat cga ttt cca tta tca tct aat ttt atg gaa	1104
Leu Thr Ile Ser Ser Asn Arg Phe Pro Leu Ser Ser Asn Phe Met Glu	
355 360 365	
tat ttt tca gga cat acg tta cgc cgt agt tat ctg aac gaa tca gca	1152
Tyr Phe Ser Gly His Thr Leu Arg Arg Ser Tyr Leu Asn Glu Ser Ala	
370 375 380	
tta caa gaa gaa agt tat ggc cta att aca acc aca aga gca aca att	1200
Leu Gln Glu Glu Ser Tyr Gly Leu Ile Thr Thr Thr Arg Ala Thr Ile	
385 390 395 400	

aat ccc gga tta gaa gga aca aac cgc ata gag tca acg gca tta gaa	1248
Asn Pro Gly Leu Glu Gly Thr Asn Arg Ile Glu Ser Thr Ala Leu Glu	
405 410 415	
ttt cgt tct gca ttg ata ggt ata tat ggc tta aat aga gct tct ttt	1296
Phe Arg Ser Ala Leu Ile Gly Ile Tyr Gly Leu Asn Arg Ala Ser Phe	
420 425 430	
tta cca gga ggc ttg ttt aat ggt acg act tct cct gct aat gga gga	1344
Leu Pro Gly Gly Leu Phe Asn Gly Thr Thr Ser Pro Ala Asn Gly Gly	
435 440 445	
tgt aga gaa ctc tat gaa aca aat gaa gaa tta cca cca gaa gaa agt	1392
Cys Arg Glu Leu Tyr Glu Thr Asn Glu Glu Leu Pro Pro Glu Glu Ser	
450 455 460	
acc gga agt tca acc cat aga cta tct cat tta acc ttt ttt agc ttt	1440
Thr Gly Ser Ser Thr His Arg Leu Ser His Leu Thr Phe Phe Ser Phe	
465 470 475 480	
caa act aat cag gct gga tct ata gct aat gca gga agt tta cct act	1488
Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Leu Pro Thr	
485 490 495	
tat tta ttt acc cgt cgt gaa tta gaa ctt aat aat acg att acc cca	1536
Tyr Leu Phe Thr Arg Arg Glu Leu Glu Leu Asn Asn Thr Ile Thr Pro	
500 505 510	
aat aga att aca caa tta cca ttg tta aag gca tct gca cct tta tcg	1584
Asn Arg Ile Thr Gln Leu Pro Leu Leu Lys Ala Ser Ala Pro Leu Ser	
515 520 525	
ggg act acg tta tta aaa ggt cca gga ttt aca gga ggg ggt ata ctc	1632
Gly Thr Thr Leu Leu Lys Gly Pro Gly Phe Thr Gly Gly Gly Ile Leu	
530 535 540	
cga aga aca act aat ggc aca ttt gga acg tta aga tta acg tta aat	1680
Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Leu Thr Leu Asn	
545 550 555 560	
tca cca tta aca caa caa tat cgc cta aga tta cgt ttt gcc tca aca	1728
Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Leu Arg Phe Ala Ser Thr	
565 570 575	
gga aat ttc agt ata agg tta ctc cgt gga ggg tta tct atc ggt gaa	1776
Gly Asn Phe Ser Ile Arg Leu Leu Arg Gly Gly Leu Ser Ile Gly Glu	
580 585 590	
tta aga tta ggg agc aca atg aac aga ggg cag gaa cta act tac gaa	1824
Leu Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu	
595 600 605	
tcc ttt ttc aca aga gag ttt act act act ggt ccg ttc aat ccg cct	1872
Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro	
610 615 620	
ttt aca ttt aca caa gct caa gag att cta aca tta aat gca gaa ggt	1920

[illegible]

Gln	Leu	Pro	Leu	Leu	Ser	Leu	Tyr	Ala	Gln	Ala	Leu	Asn	Leu	His	Leu		
	195						200					205					
Leu	Leu	Leu	Lys	Glu	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Phe	Gly	Phe	Thr		
	210					215					220						
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Glu	Arg	Gln	Leu	Glu	Leu	Thr	Ala		
225					230					235					240		
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Phe	Tyr	Asn	Thr	Gly	Leu	Glu	Arg		
			245						250						255		
Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Phe	Leu	Arg	Tyr	His	Gln	Phe	Arg		
			260					265					270				
Arg	Glu	Met	Thr	Leu	Leu	Leu	Leu	Glu	Leu	Leu	Ala	Leu	Phe	Pro	Tyr		
	275						280					285					
Tyr	Glu	Leu	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg		
	290					295					300						
Glu	Leu	Tyr	Thr	Glu	Pro	Ile	Leu	Phe	Asn	Pro	Pro	Ala	Asn	Leu	Gly		
305					310					315					320		
Leu	Cys	Arg	Arg	Phe	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu		
				325					330						335		
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Glu	Arg	Leu	Asn	Ser		
		340						345					350				
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Leu	Ser	Ser	Asn	Phe	Met	Glu		
	355						360					365					
Tyr	Phe	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Glu	Ser	Ala		
	370					375					380						
Leu	Gln	Glu	Glu	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile		
385					390					395					400		
Asn	Pro	Gly	Leu	Glu	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Leu	Glu		
			405						410						415		
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Leu	Asn	Arg	Ala	Ser	Phe		
			420					425					430				
Leu	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly		
	435						440					445					
Cys	Arg	Glu	Leu	Tyr	Glu	Thr	Asn	Glu	Glu	Leu	Pro	Pro	Glu	Glu	Ser		
	450					455					460						
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Leu	Thr	Phe	Phe	Ser	Phe		
465					470					475					480		
Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Leu	Pro	Thr		
			485					490							495		

Tyr Leu Phe Thr Arg Arg Glu Leu Glu Leu Asn Asn Thr Ile Thr Pro
 500 505 510
 Asn Arg Ile Thr Gln Leu Pro Leu Leu Lys Ala Ser Ala Pro Leu Ser
 515 520 525
 Gly Thr Thr Leu Leu Lys Gly Pro Gly Phe Thr Gly Gly Gly Ile Leu
 530 535 540
 Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Leu Thr Leu Asn
 545 550 555 560
 Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Leu Arg Phe Ala Ser Thr
 565 570 575
 Gly Asn Phe Ser Ile Arg Leu Leu Arg Gly Gly Leu Ser Ile Gly Glu
 580 585 590
 Leu Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu
 595 600 605
 Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro
 610 615 620
 Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Leu Asn Ala Glu Gly
 625 630 635 640
 Leu Ser Thr Gly Gly Glu Tyr Tyr Ile Glu Arg Ile Glu Ile Leu Pro
 645 650 655
 Leu Asn Pro Ala Arg Glu Ala Glu Glu Glu Leu Glu Ala Ala Lys Lys
 660 665 670

Ala

<210> 11
 <211> 2019
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence description: Cry9Ca1-25%

<220>
 <221> CDS
 <222> (1)..(2019)

<400> 11
 atg aat cga aat aat caa aat gaa tat gaa att att gat gcc ccc cat 48
 Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Pro His
 1 5 10 15
 tgt ggg tgt cca tca gat gac gat gtg agg tat cct ttg gca agt gac 96

Cys	Gly	Cys	Pro	Ser	Asp	Asp	Asp	Val	Arg	Tyr	Pro	Leu	Ala	Ser	Asp		
			20					25					30				
cca	aat	gca	gcg	tta	caa	aat	atg	aac	tat	aaa	gat	tac	tta	caa	atg	144	
Pro	Asn	Ala	Ala	Leu	Gln	Asn	Met	Asn	Tyr	Lys	Asp	Tyr	Leu	Gln	Met		
		35					40					45					
aca	gat	gag	gac	tac	act	gat	tct	tat	ata	aat	cct	agt	tta	tct	att	192	
Thr	Asp	Glu	Asp	Tyr	Thr	Asp	Ser	Tyr	Ile	Asn	Pro	Ser	Leu	Ser	Ile		
	50					55					60						
agt	ggt	aga	gaa	gca	tta	cag	act	gcg	ctt	acg	tta	tta	ggg	aga	ata	240	
Ser	Gly	Arg	Glu	Ala	Leu	Gln	Thr	Ala	Leu	Thr	Leu	Leu	Gly	Arg	Ile		
	65				70				75						80		
ctc	ggg	gct	tta	ggt	gtt	cgg	ttt	tct	gga	caa	ata	tta	agt	ttt	tat	288	
Leu	Gly	Ala	Leu	Gly	Val	Pro	Phe	Ser	Gly	Gln	Ile	Leu	Ser	Phe	Tyr		
			85					90						95			
caa	ttc	ctt	tta	aat	aca	ctg	tgg	cca	gtt	aat	gat	aca	gct	ata	tgg	336	
Gln	Phe	Leu	Leu	Asn	Thr	Leu	Trp	Pro	Val	Asn	Asp	Thr	Ala	Ile	Trp		
			100					105					110				
gaa	gct	ttc	atg	cga	cag	gtg	gag	gaa	ctt	gtc	aat	caa	caa	ata	aca	384	
Glu	Ala	Phe	Met	Arg	Gln	Val	Glu	Glu	Leu	Val	Asn	Gln	Gln	Ile	Thr		
		115					120					125					
gaa	ttt	gca	aga	aat	cag	gca	ctt	gca	aga	ttg	caa	gga	tta	gga	gaa	432	
Glu	Phe	Ala	Arg	Asn	Gln	Ala	Leu	Ala	Arg	Leu	Gln	Gly	Leu	Gly	Glu		
	130					135					140						
tct	ttt	aat	gta	tat	caa	cgt	tcc	ctt	caa	aat	tgg	ttg	gct	gat	cga	480	
Ser	Phe	Asn	Val	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Trp	Leu	Ala	Asp	Arg		
	145				150					155					160		
aat	gat	aca	cga	aat	tta	agt	tta	tta	cgt	gct	caa	ttt	ata	gct	tta	528	
Asn	Asp	Thr	Arg	Asn	Leu	Ser	Leu	Leu	Arg	Ala	Gln	Phe	Ile	Ala	Leu		
				165					170					175			
gac	ctt	gat	ttt	gtt	aat	gct	att	cca	ttg	ttt	gca	gta	aat	gga	cag	576	
Asp	Leu	Asp	Phe	Val	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Val	Asn	Gly	Gln		
			180					185					190				
cag	gtt	cca	tta	ctg	tca	gta	tat	gca	caa	gct	tta	aat	tta	cat	ttg	624	
Gln	Val	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Leu	Asn	Leu	His	Leu		
		195					200					205					
tta	tta	tta	aaa	gaa	gca	tct	ctt	ttt	gga	gaa	gga	tggt	gga	ttc	aca	672	
Leu	Leu	Leu	Lys	Glu	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Trp	Gly	Phe	Thr		
	210					215					220						
cag	ggg	gaa	att	tcc	aca	tat	tat	gaa	cgt	caa	ttg	gaa	cta	acc	gct	720	
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Glu	Arg	Gln	Leu	Glu	Leu	Thr	Ala		
	225				230					235					240		
aag	tac	act	aat	tac	tgt	gaa	act	tgg	tat	aat	aca	ggt	tta	gaa	cgt	768	
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Trp	Tyr	Asn	Thr	Gly	Leu	Glu	Arg		

245										250					255					
tta	aga	gga	aca	aat	act	gaa	agt	ttt	tta	aga	tat	cat	caa	ttc	cgt	816				
Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Phe	Leu	Arg	Tyr	His	Gln	Phe	Arg					
			260				265						270							
aga	gaa	atg	act	tta	gtg	gta	tta	gat	gtt	gtg	gcg	cta	ttt	cca	tat	864				
Arg	Glu	Met	Thr	Leu	Val	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Tyr					
			275				280						285							
tat	gat	gta	cga	ctt	tat	cca	acg	gga	tca	aac	cca	cag	ctt	aca	cgt	912				
Tyr	Asp	Val	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg					
			290				295						300							
gag	gta	tat	aca	gat	ccg	att	gta	ttt	aat	cca	cca	gct	aat	tta	gga	960				
Glu	Val	Tyr	Thr	Asp	Pro	Ile	Val	Phe	Asn	Pro	Pro	Ala	Asn	Leu	Gly					
305						310						315			320					
ctt	tgc	cga	cgt	tgg	ggg	act	aat	ccc	tat	aat	act	ttt	tct	gag	ctc	1008				
Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu					
			325						330						335					
gaa	aat	gcc	ttc	att	cgc	cca	cca	cat	ctt	ttt	gaa	agg	ctg	aat	agc	1056				
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Glu	Arg	Leu	Asn	Ser					
			340						345						350					
tta	aca	atc	agc	agt	aat	cga	ttt	cca	gtt	tca	tct	aat	ttt	atg	gaa	1104				
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	Met	Glu					
			355						360						365					
tat	ttt	tca	gga	cat	acg	tta	cgc	cgt	agt	tat	ctg	aac	gat	tca	gca	1152				
Tyr	Phe	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala					
370						375						380								
gta	caa	gaa	gat	agt	tat	ggc	cta	att	aca	acc	aca	aga	gca	aca	att	1200				
Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile					
385						390						395			400					
aat	ccc	gga	gtt	gat	gga	aca	aac	cgc	ata	gag	tca	acg	gca	gta	gat	1248				
Asn	Pro	Gly	Val	Asp	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Val	Asp					
			405						410						415					
ttt	cgt	tct	gca	ttg	ata	ggg	ata	tat	ggc	gtg	aat	aga	gct	tct	ttt	1296				
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	Ser	Phe					
			420						425						430					
gtc	cca	gga	ggc	ttg	ttt	aat	ggg	acg	act	tct	cct	gct	aat	gga	gga	1344				
Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly					
			435						440						445					
tgt	aga	gat	ctc	tat	gat	aca	aat	gat	gaa	tta	cca	cca	gat	gaa	agt	1392				
Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser					
450						455						460								
acc	gga	agt	tca	acc	cat	aga	cta	tct	cat	tta	acc	ttt	ttt	agc	ttt	1440				
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Leu	Thr	Phe	Phe	Ser	Phe					
465						470						475			480					

caa act aat cag gct gga tct ata gct aat gca gga agt gta cct act	1488
Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Val Pro Thr	
485 490 495	
tat gtt tgg acc cgt cgt gat gtg gac ctt aat aat acg att acc cca	1536
Tyr Val Trp Thr Arg Arg Asp Val Asp Leu Asn Asn Thr Ile Thr Pro	
500 505 510	
aat aga att aca caa tta cca ttg gta aag gca tct gca cct gtt tcg	1584
Asn Arg Ile Thr Gln Leu Pro Leu Val Lys Ala Ser Ala Pro Val Ser	
515 520 525	
ggt act acg gtc tta aaa ggt cca gga ttt aca gga ggg ggt ata ctc	1632
Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly Gly Gly Ile Leu	
530 535 540	
cga aga aca act aat ggc aca ttt gga acg tta aga gta acg gtt aat	1680
Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Val Thr Val Asn	
545 550 555 560	
tca cca tta aca caa caa tat cgc cta aga tta cgt ttt gcc tca aca	1728
Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Leu Arg Phe Ala Ser Thr	
565 570 575	
gga aat ttc agt ata agg gta ctc cgt gga ggg gtt tct atc ggt gat	1776
Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp	
580 585 590	
gtt aga tta ggg agc aca atg aac aga ggg cag gaa cta act tac gaa	1824
Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu	
595 600 605	
tcc ttt ttc aca aga gag ttt act act act ggt ccg ttc aat ccg cct	1872
Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro	
610 615 620	
ttt aca ttt aca caa gct caa gag att cta aca gtg aat gca gaa ggt	1920
Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly	
625 630 635 640	
gtt agc acc ggt ggt gaa tat tat ata gat aga att gaa att gtc cct	1968
Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro	
645 650 655	
gtg aat ccg gca cga gaa gcg gaa gag gat tta gaa gcg gcg aag aaa	2016
Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Ala Ala Lys Lys	
660 665 670	
gcg	2019
Ala	

<210> 12

<211> 673

<212> PRT

<213> Artificial sequence

<223> Artificial sequence description: Cry9Ca1-25%

<400> 12

Met	Asn	Arg	Asn	Asn	Gln	Asn	Glu	Tyr	Glu	Ile	Ile	Asp	Ala	Pro	His
1				5					10					15	
Cys	Gly	Cys	Pro	Ser	Asp	Asp	Asp	Val	Arg	Tyr	Pro	Leu	Ala	Ser	Asp
			20					25					30		
Pro	Asn	Ala	Ala	Leu	Gln	Asn	Met	Asn	Tyr	Lys	Asp	Tyr	Leu	Gln	Met
		35					40					45			
Thr	Asp	Glu	Asp	Tyr	Thr	Asp	Ser	Tyr	Ile	Asn	Pro	Ser	Leu	Ser	Ile
	50					55					60				
Ser	Gly	Arg	Glu	Ala	Leu	Gln	Thr	Ala	Leu	Thr	Leu	Leu	Gly	Arg	Ile
65					70					75					80
Leu	Gly	Ala	Leu	Gly	Val	Pro	Phe	Ser	Gly	Gln	Ile	Leu	Ser	Phe	Tyr
			85						90					95	
Gln	Phe	Leu	Leu	Asn	Thr	Leu	Trp	Pro	Val	Asn	Asp	Thr	Ala	Ile	Trp
		100						105					110		
Glu	Ala	Phe	Met	Arg	Gln	Val	Glu	Glu	Leu	Val	Asn	Gln	Gln	Ile	Thr
	115						120					125			
Glu	Phe	Ala	Arg	Asn	Gln	Ala	Leu	Ala	Arg	Leu	Gln	Gly	Leu	Gly	Glu
130					135						140				
Ser	Phe	Asn	Val	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Trp	Leu	Ala	Asp	Arg
145					150					155					160
Asn	Asp	Thr	Arg	Asn	Leu	Ser	Leu	Leu	Arg	Ala	Gln	Phe	Ile	Ala	Leu
				165					170					175	
Asp	Leu	Asp	Phe	Val	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Val	Asn	Gly	Gln
		180						185					190		
Gln	Val	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Leu	Asn	Leu	His	Leu
	195						200					205			
Leu	Leu	Leu	Lys	Glu	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Trp	Gly	Phe	Thr
210						215					220				
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Glu	Arg	Gln	Leu	Glu	Leu	Thr	Ala
225					230					235					240
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Trp	Tyr	Asn	Thr	Gly	Leu	Glu	Arg
			245						250					255	
Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Phe	Leu	Arg	Tyr	His	Gln	Phe	Arg
		260						265					270		
Arg	Glu	Met	Thr	Leu	Val	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Tyr
	275						280					285			

Tyr Asp Val Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu Thr Arg
290 295 300
Glu Val Tyr Thr Asp Pro Ile Val Phe Asn Pro Pro Ala Asn Leu Gly
305 310 315 320
Leu Cys Arg Arg Trp Gly Thr Asn Pro Tyr Asn Thr Phe Ser Glu Leu
325 330 335
Glu Asn Ala Phe Ile Arg Pro Pro His Leu Phe Glu Arg Leu Asn Ser
340 345 350
Leu Thr Ile Ser Ser Asn Arg Phe Pro Val Ser Ser Asn Phe Met Glu
355 360 365
Tyr Phe Ser Gly His Thr Leu Arg Arg Ser Tyr Leu Asn Asp Ser Ala
370 375 380
Val Gln Glu Asp Ser Tyr Gly Leu Ile Thr Thr Thr Arg Ala Thr Ile
385 390 395 400
Asn Pro Gly Val Asp Gly Thr Asn Arg Ile Glu Ser Thr Ala Val Asp
405 410 415
Phe Arg Ser Ala Leu Ile Gly Ile Tyr Gly Val Asn Arg Ala Ser Phe
420 425 430
Val Pro Gly Gly Leu Phe Asn Gly Thr Thr Ser Pro Ala Asn Gly Gly
435 440 445
Cys Arg Asp Leu Tyr Asp Thr Asn Asp Glu Leu Pro Pro Asp Glu Ser
450 455 460
Thr Gly Ser Ser Thr His Arg Leu Ser His Leu Thr Phe Phe Ser Phe
465 470 475 480
Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Val Pro Thr
485 490 495
Tyr Val Trp Thr Arg Arg Asp Val Asp Leu Asn Asn Thr Ile Thr Pro
500 505 510
Asn Arg Ile Thr Gln Leu Pro Leu Val Lys Ala Ser Ala Pro Val Ser
515 520 525
Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly Gly Gly Ile Leu
530 535 540
Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Val Thr Val Asn
545 550 555 560
Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Leu Arg Phe Ala Ser Thr
565 570 575
Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp
580 585 590

Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu
595 600 605

Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro
610 615 620

Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly
625 630 635 640

Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro
645 650 655

Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Ala Ala Lys Lys
660 665 670

Ala

<210> 13
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: mutant 1

<400> 13
gaattaaatg aattttttaa tttaagtgtt 30

<210> 14
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: mutant 2

<400> 14
gaattaaatg aattattaaa tttaagtgtt 30

<210> 15
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: mutant 3

<400> 15
gaattattag aattttttatt attaagtgtt 30

<210> 16

<211> 30
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Artificial sequence description: mutant 4

 <400> 16
 gaattattag aattattatt attaagtggt 30

<210> 17
 <211> 30
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Artificial sequence description: mutant 5

 <400> 17
 gaattattag aagaattatt attaagtggt 30

<210> 18
 <211> 30
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Artificial sequence description: mutant 6

 <400> 18
 gaacgattag aattttttatt attaagtggt 30

<210> 19
 <211> 30
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Artificial sequence description: mutant 7

 <400> 19
 gaacgattag aattattatt attaagtggt 30

<210> 20
 <211> 30
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Artificial sequence description: mutant 8

 <400> 20
 gaattagaag aattattatt attaagtggt 30

<210> 21
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: mutant 9

<400> 21
gaattattag aagaagaaga attaagtgtt 30

<210> 22
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: mutant 10

<400> 22
tttttattaa atttattttt tttaccatta ctg 33

<210> 23
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: mutant11

<400> 23
tttttattaa atttagaaga attaccatta ctg 33

<210> 24
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: mutant 12

<400> 24
tttgaagaaa atttagaaga attaccatta ctg 33

<210> 25
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: mutant 13

<400> 25
tttgaagaaa attttttatt atttccatta ctg 33

<210> 26
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: mutant 14

<400> 26
tttgaagaaa attttgaaga atttccatta ctg 33

<210> 27
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: mutant 15

<400> 27
tttttattaa attttgaaga atttccatta ctg 33

<210> 28
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: mutant 16

<400> 28
tttttattaa atgaattttt tgaaccatta ctg 33

<210> 29
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: mutant 17

<400> 29
cttttttttag aattattttt attc 24

<210> 30
<211> 24
<212> DNA
<213> Artificial sequence

<220>
 <223> Artificial sequence description: mutant 18

 <400> 30
 ctttttttat tattattttt attc 24

 <210> 31
 <211> 24
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Artificial sequence description: mutant 19

 <400> 31
 ctttttttag aagaatttga atta 24

 <210> 32
 <211> 24
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Artificial sequence description: mutant 20

 <400> 32
 ctttttgaag aagaatttga atta 24

 <210> 33
 <211> 24
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Artificial sequence description: mutant 21

 <400> 33
 ctttttgaag aattatttga agaa 24

 <210> 34
 <211> 15
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Artificial sequence description: mutant 22

 <400> 34
 ttattagaat taaat 15

 <210> 35

<211> 15
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: mutant 23

<400> 35
ttattatttt taaat 15

<210> 36
<211> 15
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: mutant 24

<400> 36
ttagaattat taaat 15

<210> 37
<211> 15
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: mutant 25

<400> 37
ttattatttt ttaat 15

<210> 38
<211> 15
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: mutant 26

<400> 38
ttagaagaat taaat 15

<210> 39
<211> 15
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: mutant 27

<400> 39
ttagaatttt taaat 15

<210> 40
<211> 15
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: mutant 28

<400> 40
ttagaatttg aaaat 15

<210> 41
<211> 15
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: mutant 29

<400> 41
ttagaagaag aaaat 15

<210> 42
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 1

<400> 42
gatcgaaatg atacattaaa tttaagtgtt gtt 33

<210> 43
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 2

<400> 43
gatcgaaatg atacatttaa tttaagtgtt gtt 33

<210> 44
<211> 33
<212> DNA
<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 3

<400> 44

gatcgaaatg atacagaaaa tttaagtgtt gtt

33

<210> 45

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 4

<400> 45

cgaaatgata cacgattatt aagtgttggtt cgt

33

<210> 46

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 5

<400> 46

cgaaatgata caccagaatt aagtgttggtt cgt

33

<210> 47

<211> 39

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 6

<400> 47

ttggctgac gaaatgaatt tttaaattta agtgttggtt

39

<210> 48

<211> 39

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 7

<400> 48

ttggctgatac gaaatgaatt tttattatta agtggtggt 39

<210> 49

<211> 39

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 8

<400> 49

ttggctgatac gaaatgaatt attaaattta agtggtggt 39

<210> 50

<211> 39

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 9

<400> 50

ttggctgatac gaaatgaatt attattatta agtggtggt 39

<210> 51

<211> 39

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 10

<400> 51

ttggctgatac gaaatgaaga agaagaatta agtggtggt 39

<210> 52

<211> 39

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 11

<400> 52

ttggctgatac gaaatgaaga attattatta agtggtggt 39

<210> 53

<211> 36

<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 12

<400> 53
caaaattggt tggctgaatt aaatgaatta ttaaatt 36

<210> 54
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 13

<400> 54
caaaattggt tggctgaatt aaatgaattt ttaaatt 36

<210> 55
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 14

<400> 55
caaaattggt tggctgaatt attagaattt ttattatta 39

<210> 56
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 15

<400> 56
caaaattggt tggctgaatt attagaatta ttattatta 39

<210> 57
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:

oligonucleotide 16

<400> 57
caaaattggt tggctgaatt attagaagaa ttattatta 39

<210> 58
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 17

<400> 58
caaaattggt tggctgaacg attagaattt ttattatta 39

<210> 59
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 18

<400> 59
caaaattggt tggctgaacg attagaatta ttattatta 39

<210> 60
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 19

<400> 60
caaaattggt tggctgaatt agaagaatta ttattatta 39

<210> 61
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 20

<400> 61
caaaattggt tggctgaatt attagaagaa gaagaatta 39

<210> 62
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 21

<400> 62
gctattccat tgttttttatt aaatggacag caggtt 36

<210> 63
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 22

<400> 63
gctattccat tgtttgaaga aaatggacag caggtt 36

<210> 64
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 23

<400> 64
ttattaaatg gacagcagtt accattactg tcagta 36

<210> 65
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 24

<400> 65
ttattaaatg gacagcagtt tccattactg tcagta 36

<210> 66
<211> 36
<212> DNA
<213> Artificial sequence

<220>
 <223> Artificial sequence description:
 oligonucleotide 25

<400> 66
 ttattaaatg gacagcagga accattactg tcagta 36

<210> 67
 <211> 36
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence description:
 oligonucleotide 26

<400> 67
 gaagaaaatg gacagcagtt accattactg tcagta 36

<210> 68
 <211> 36
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence description:
 oligonucleotide 27

<400> 68
 gaagaaaatg gacagcagtt tccattactg tcagta 36

<210> 69
 <211> 45
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence description:
 oligonucleotide 28

<400> 69
 ccattgtttt tattaaattt atttttttta ccattactgt cagta 45

<210> 70
 <211> 45
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence description:
 oligonucleotide 29

<400> 70
ccattgtttt tattaaattt agaagaatta ccattactgt cagta 45

<210> 71
<211> 45
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 30

<400> 71
ccattgtttg aagaaaattt agaagaatta ccattactgt cagta 45

<210> 72
<211> 45
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 31

<400> 72
ccattgtttg aagaaaattt tttattattt ccattactgt cagta 45

<210> 73
<211> 45
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 32

<400> 73
ccattgtttg aagaaaattt tgaagaattt ccattactgt cagta 45

<210> 74
<211> 45
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 33

<400> 74
ccattgtttt tattaaattt tgaagaattt ccattactgt cagta 45

<210> 75

<211> 45
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 34

<400> 75
ccattgtttt tattaaatga attttttgaa ccattactgt cagta 45

<210> 76
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 35

<400> 76
gatgcatctc tttttttaga aggatgggga ttc 33

<210> 77
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 36

<400> 77.
gatgcatctc tttttttatt aggatgggga ttcaca 36

<210> 78
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 37

<400> 78
gatgcatctc tttttgaaga aggatgggga ttc 33

<210> 79
<211> 33
<212> DNA
<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 38

<400> 79
ttagaaggat ggggattaac acaggggggaa att 33

<210> 80
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 39

<400> 80
gaagaaggat ggggagaaac acaggggggaa att 33

<210> 81
<211> 45
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 40

<400> 81
gcatctcttt ttttagaatt atttttattc acacaggggg aaatt 45

<210> 82
<211> 45
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 41

<400> 82
gcatctcttt ttttattatt atttttattc acacaggggg aaatt 45

<210> 83
<211> 45
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 42

<400> 83
gcatctcttt ttttagaatt atttttattc acacaggggg aaatt 45

<210> 84
<211> 45
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 43

<400> 84
gcacatctcttt ttgaagaatt atttttattc acacaggggg aaatt 45

<210> 85
<211> 45
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 44

<400> 85
gcacatctcttt ttgaagaatt attttttagaa acacaggggg aaatt 45

<210> 86
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 45

<400> 86
ggtttagatc gtttattaga attaaatact gaaagttgg 39

<210> 87
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 46

<400> 87
ggtttagatc gtttattatt tttaaatact gaaagttgg 39

<210> 88
<211> 39
<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 47

<400> 88

ggtttagatc gtttagaatt attaaatact gaaagttgg

39

<210> 89

<211> 39

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 48

<400> 89

ggtttagatc gtttattatt ttttaatact gaaagttgg

39

<210> 90

<211> 39

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 49

<400> 90

ggtttagatc gtttagaaga attaaatact gaaagttgg

39

<210> 91

<211> 39

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 50

<400> 91

ggtttagatc gtttagaatt ttttaatact gaaagttgg

39

<210> 92

<211> 39

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 51

<400> 92
ggtttagatc gtttagaatt tgaaaatact gaaagttgg 39

<210> 93
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 52

<400> 93
ggtttagatc gtttagaaga agaaaatact gaaagttgg 39

<210> 94
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 53

<400> 94
tgaatatgaa attattgaag cccccattg 30

<210> 95
<211> 40
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 54

<400> 95
tggtgtcca tcagaagaag aattaaggta tcctttggca 40

<210> 96
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 55

<400> 96
tcctttggca agtgaaccaa atgcagc 27

<210> 97
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 56

<400> 97
gaactataaa gaatacttac aaatg 25

<210> 98
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 57

<400> 98
caaatgacag aagaggaata cactga 26

<210> 99
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 58

<400> 99
tacactgaat cttatataaa 20

<210> 100
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 59

<400> 100
tattagtggg agagaagcat tacagactgc gcttac 36

<210> 101
<211> 37
<212> DNA
<213> Artificial sequence

<220>
 <223> Artificial sequence description:
 oligonucleotide 60

 <400> 101
 cagactgcgc ttactgttat tagggagaat actcggg 37

<210> 102
 <211> 25
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence description:
 oligonucleotide 61

 <400> 102
 gggctttagg tttaccgttt tctgg 25

<210> 103
 <211> 28
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence description:
 oligonucleotide 62

 <400> 103
 ttctggacaa atattaagtt tttatcaa 28

<210> 104
 <211> 40
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence description:
 oligonucleotide 63

 <400> 104
 cttttaaata cactgtttcc attaaatgaa acagctatat 40

<210> 105
 <211> 24
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence description:
 oligonucleotide 64

 <400> 105

acagctatat ttgaagcttt catg 24

<210> 106

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 65

<400> 106

ctttcatgcg acagtttagag gaactt 26

<210> 107

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 66

<400> 107

gaggaacttt taaatcaaca aataac 26

<210> 108

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 67

<400> 108

ggattaggag aatcttttaa t 21

<210> 109

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 68

<400> 109

tcttttaatt tatatcaacg ttc 23

<210> 110

<211> 21

<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 69

<400> 110
ccttcaaaat tttttggctg a 21

<210> 111
<211> 17
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 70

<400> 111
ttggctgaac gaaatga 17

<210> 112
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 71

<400> 112
cgaaatgaaa cacgaaattt aag 23

<210> 113
<211> 37
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 72

<400> 113
acacgaaatt taagtttatt acgtgctcaa tttatag 37

<210> 114
<211> 48
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:

oligonucleotide 73

<400> 114
gctcaattta tagctttaga acttgaattt ttaaagtcta ttccattg 48

<210> 115
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 74

<400> 115
ccattgtttg cattaaatgg acagcag 27

<210> 116
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 75

<400> 116
ccattgtttg cattaaatgg acagcag 27

<210> 117
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 76

<400> 117
ccattactgt cattatatgc acaagct 27

<210> 118
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 77

<400> 118
tatgcacaag ctttaaattt acatttg 27

<210> 119
 <211> 23
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Artificial sequence description:
 oligonucleotide 78

 <400> 119
 ttattaaaaag aagcatctct ttt

23

<210> 120
 <211> 25
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Artificial sequence description:
 oligonucleotide 79

 <400> 120
 tggagaagga tttggattca cacag

25

<210> 121
 <211> 24
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Artificial sequence description:
 oligonucleotide 80

 <400> 121
 cacatattat gaacgtcaat tgga

24

<210> 122
 <211> 28
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Artificial sequence description:
 oligonucleotide 81

 <400> 122
 tactgtgaaa ctttttataa tacaggtt

28

<210> 123
 <211> 25
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence description:
 oligonucleotide 82

 <400> 123
 tacaggttta gaacgtttaa gagga 25

<210> 124
 <211> 28
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence description:
 oligonucleotide 83

 <400> 124
 aatactgaaa gttttttaag atatcatc 28

<210> 125
 <211> 51
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence description:
 oligonucleotide 84

 <400> 125
 gtagagaaat gactttatta ttattagaat tattagcgct atttccatat t 51

<210> 126
 <211> 27
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence description:
 oligonucleotide 85

 <400> 126
 atattatgaa ttacgacttt atccaac 27

<210> 127
 <211> 23
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence description:
 oligonucleotide 86

<400> 127
cttacacgtg agttatatac aga 23

<210> 128
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 87

<400> 128
tatacagaac cgatttttatt taatccacc 29

<210> 129
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 88

<400> 129
ccaccagcta atttaggact ttgccgac 28

<210> 130
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 89

<400> 130
ctttgccgac gttttggtac taatccc 27

<210> 131
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 90

<400> 131
catctttttg aaaggctgaa tag 23

<210> 132

<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 91

<400> 132
taatcgattt ccattatcat ctaattttat 30

<210> 133
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 92

<400> 133
ctaattttat ggaatatattt tcaggacata cgttac 36

<210> 134
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 93

<400> 134
tagttatctg aacgaatcag cattacaaga aga 33

<210> 135
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 94

<400> 135
caagaagaaa gttatggcct 20

<210> 136
<211> 35
<212> DNA
<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 95

<400> 136
caattaatcc cggattagaa ggaacaaacc gcata 35

<210> 137
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 96

<400> 137
gagtcaacgg cattagaatt tcgttctgca 30

<210> 138
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 97

<400> 138
ggtatatatg gcttaaataag agcttc 26

<210> 139
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 98

<400> 139
tagagcttct tttttaccag gaggcttggt 30

<210> 140
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 99

<400> 140
ctgctaattg aggatgtaga gaactctatg a 31

<210> 141
<211> 17
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 100

<400> 141
ctctatgaaa caaatga

17

<210> 142
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 101

<400> 142
acaaatgaag aattaccacc

20

<210> 143
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 102

<400> 143
attaccacca gaagaaagta ccggaag

27

<210> 144
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 103

<400> 144
agactatctc atttaacctt ttttagcttt

30

<210> 145
<211> 27
<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 104

<400> 145

gctaatagcag gaagtttacc tacttat

27

<210> 146

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 105

<400> 146

cctacttatt tatTTaccCG tcgtga

26

<210> 147

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 106

<400> 147

accCGtcgtg aattagaact taataatacg att

33

<210> 148

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 107

<400> 148

attaccattg ttAAaggcat ctgc

24

<210> 149

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 108

<p><400> 149 aaggcatctg cacctttatc gggactacg</p>	30
<p><210> 150 <211> 29 <212> DNA <213> Artificial sequence</p>	
<p><220> <223> Artificial sequence description: oligonucleotide 109</p>	
<p><400> 150 tcgggtacta cgttattaaa aggtccagg</p>	29
<p><210> 151 <211> 40 <212> DNA <213> Artificial sequence</p>	
<p><220> <223> Artificial sequence description: oligonucleotide 110</p>	
<p><400> 151 acatttgga cgttaagatt aacgttaa taccattaa</p>	40
<p><210> 152 <211> 37 <212> DNA <213> Artificial sequence</p>	
<p><220> <223> Artificial sequence description: oligonucleotide 111</p>	
<p><400> 152 cacaacaata tcgcctaaga ttacgttttg cctcaac</p>	37
<p><210> 153 <211> 31 <212> DNA <213> Artificial sequence</p>	
<p><220> <223> Artificial sequence description: oligonucleotide 112</p>	
<p><400> 153 aaatttcagt ataagggtac tccgtggagg g</p>	31

<210> 154
 <211> 35
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Artificial sequence description:
 oligonucleotide 113

 <400> 154
 ataagggtac tccgtggagg gttatctatc ggtga 35

 <210> 155
 <211> 29
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Artificial sequence description:
 oligonucleotide 114

 <400> 155
 tctatcggtg aattaagatt agggagcac 29

 <210> 156
 <211> 30
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Artificial sequence description:
 oligonucleotide 115

 <400> 156
 caagagattc taacattaa tgcagaaggt 30

 <210> 157
 <211> 32
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Artificial sequence description:
 oligonucleotide 116

 <400> 157
 aatgcagaag gtttaagcac cggtggtgaa ta 32

 <210> 158
 <211> 32
 <212> DNA
 <213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 117

<400> 158
gtggtgaata ttatatagaa agaattgaaa tt

32

<210> 159
<211> 37
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 118

<400> 159
agaattgaaa ttttaccttt aaatccggca cgagaag

37

<210> 160
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 119

<400> 160
cgagaagcgg aagaggaatt agaagcggcg
1

30